SEQUENCE LISTING

- (1) GENERAL INFORMATION
- (i) APPLICANT: Wei-Wu He, Kristine K. Kikly, Vishva M. Dixit, Steven M. Ruben
- (ii) TITLE OF THE INVENTION: INTERLEUKIN-1 BETA CONVERTING ENZYME LIKE APOPTOSIS PROTESE-6
 - (iii) NUMBER OF SEQUENCES: 9
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: SmithKline Beecham Corporation
 - (B) STREET: 709 Swedeland Road
 - (C) CITY: King of Prussia
 - (D) STATE: PA
 - (E) COUNTRY: USA
 - (F) ZIP: 19406-2799
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskedte
 - (B) COMPUTER: IBM Compactble
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ Version 1.5
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: UNKNOWN
 - (B) FILING DATE: HEREWITH
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 60/018,961
 - (B) FILING DATE: 05 JUNE 1996
 - (A) APPLICATION NUMBER: 60/020,344
 - (B) FILING DATE: 23 MAY 1996
 - (A) APPLICATION NUMBER: 60/017,949
 - (B) FILING DATE: 20 May 1996
 - (viii) ATTORNEY/AGENT INFORMATION:



- (A) NAME: Han, William T.
- (B) REGISTRATION NUMBER: 34,344
- (C) REFERENCE/DOCKET NUMBER: P50483-2

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 610-270-5219
- (B) TELEFAX: 610-270-5090
- (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 416 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO

130

- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Asp Glu Ala Asp Arg Arg Leu Leu Arg Arg Cys Arg Leu Arg Leu 10 Val Glu Glu Leu Gln Val Asp Gln Leu Trp Asp Val Leu Leu Ser Arg Glu Leu Phe Arg Pro His Met Ile Glu Asp Ile Gln Arg Ala Gly Ser 40 Gly Ser Arg Arg Asp Gln Ala Arg Gln Leu Ile Ile Asp Leu Glu Thr 55 Arg Gly Ser Gln Ala Leu Pro Leu Phe Ile Ser Cys Leu Glu Asp Thr 75 70 Gly Gln Asp Met Leu Ala Ser Phe Leu Arg Thr Asn Arg Gln Ala Gly 90. 85 Lys Leu Ser Lys Pro Thr Leu Glu Asn Leu Thr Pro Val Val Leu Arg 105 100 Pro Glu Ile Arg Lys Pro Glu Val Leu Arg Pro Glu Thr Pro Arg Pro 120 Val Asp Ile Gly Ser Gly Gly Phe Gly Asp Val Gly Ala Leu Glu Ser

135

In Pro Cys
Leu Arg Gly Asn La Asp Leu Ala Tyr Ile Leu Ser Me lu Pro Cys
145 Gly His Cys Leu Ile Ile Asn Asn Val Asn Phe Cys Arg Glu Ser Gly 170 175
Leu Arg Thr Arg Thr Gly Ser Asn Ile Asp Cys Glu Lys Leu Arg Arg 190
Arg Phe Ser Ser Leu His Phe Met Val Glu Val Lys Gly Asp Leu Thr
195 Ala Lys Lys Met Val Leu Ala Leu Leu Glu Leu Ala Arg Gln Asp His 220 220
210 215 Gly Ala Leu Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln 235 240
225 230 255 Ala Ser His Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys 250 255
245 Pro Val Ser Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys 270
260 203 Pro Ser Leu Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly 285
275 Gly Glu Gln Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu 300
290 295 Asp Glu Ser Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln 315 320
305 Glu Gly Leu Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro 330 330 335
The Ser Asp Tie Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val
Arg Asp Pro Lys Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp
(61)
Asp Ile Phe Glu Gln Trp Ala His Ser Glu Asp Leu Gln Ser Leu Leu
370 375 Leu Arg Val Ala Asn Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met 395 400
Pro Gly Cys Phe Asn Phe Leu Arg Lys Lys Led File 1115 115
405

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1578 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA



- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

THE STREET CONTROL GETGGAAGAG	60
GCCATGGACG AAGCGGATCG GCGGCTCCTG CGGCGGTGCC GGCTGCGGCT GGTGGAAGAG	120
	180
	240
	300
ATAGATCTGG AGACTCGAGG GAGTCAGGCT CTTCGTTTCTG ACAGGCCAGG ACATGCTGGC TTCGTTTCTG CGAACTAACA GGCAAGCAGG AAAGTTGTCG ACAGGCCAGG ACATGCTGGC CAGAGATTCG CAAACCAGAG	360
ACAGGCCAGG ACATGCTGGC TTCGTTTCTG CAMACTAGAC CAGAGATTCG CAAACCAGAG AAGCCAACCC TAGAAAACCT TACCCCAGTG GTGCTCGTT CTGGAGGATT CGGTGATGTC	420
AAGCCAACCC TAGAAAACCT TACCCCAGIG GIGGTOTT CTGGAGGATT CGGTGATGTC GTTCTCAGAC CGGAAACACC CAGACCAGTG GACATTGGTT ACATCCTGAG CATGGAGCCC	480
GTTCTCAGAC CGGAAACACC CAGACCAGTG GACTTTGGCT ACATCCTGAG CATGGAGCCC GGTGCTCTTG AGAGTTTGAG GGGAAATGCA GATTTGGCC GTGAGTCCGG GCTCCGCACC	540
GGTGCTCTTG AGAGTTTGAG GGGAAATGCA GATTTOTGCC GTGAGTCCGG GCTCCGCACC TGTGGCCACT GCCTCATTAT CAACAATGTG AACTTCTGCC GCTGAGTCCTC GCTGCATTTC CGCACTGGCT CCAACATCGA CTGTGAGAAG TTGCGGCGTC GCTTCTCCTC GCTGGAGCTG	600
CGCACTGGCT CCAACATCGA CTGTGAGAAG TIGCGGCCTO TGCTGGCTTT GCTGGAGCTG ATGGTGGAGG TGAAGGGCGA CCTGACTGCC AAGAAAATGG TGCTGGCTTT TCACGGCTGT	660
ATGGTGGAGG TGAAGGGCGA CCTGACTGCC AAGAAAATTOO TCACTGTCTC TCACGGCTGT GCGCGGCAGG ACCACGGTGC TCTGGACTGC TGCTACGGCA CAGATGGATG CCCTGTGTCG	720
	780
	840
	900
	960
	1020
	1080
	1140
	1200
	1260
	1320
	1380
	1440
=== AddCCTCTA TTTA ALGIGG NOTE	1500
GGAGGAAGAG GGACAGATGA ATGCCGIGGA TIGGITGTTGG TCTCTAGGAG CAGGGATTAA CCAGGGCTAG TGACTTGGTG TCCCATGATC CCTGTGTTGG TCTCTAGGAG CAGGGATTAA	1560
	1578
CCTCTGCACT ACTGACAT	

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA





- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTGACTGCCA AGAAAATGGT	GCTGGCTTTG	CTGGAGCTGG	CGCGGCAGGA	CCACGGTGCT	60
CTGGACTGCT GCGTGGTGGT	CATTCTCTCT	CACGGCTGTC	AGGCCAGCCA	CCTGCAGTTC	120
CCAGGGGCTG TCTACGGCAG	AGATGGATGC	CCTGTGTCGG	TCGAAAAGAT	TGTGAACATC	180
TTCAATGGGA CCAGCTGCCC	CAGCCTGGGA	GGGAAGCCCA	AGCTCTTTTT	CATCCAGGCC	240
TGTGGTGGGG AGCAGAAAG	CCATGGGTTT	GAGGTGGCCT	CCACTTCCCC	TGAAGACGAG	300
TCCCCTGGCA GTAACCCCG	A GCCAGATGCC	ACCCCGTTCC	AGGAAGGTTT	GAGGACCTTC	360
GACCAGCTGG ACGCCATATO	TAGTTTGCCC	ACACCCAGTG	ACATCTTTGT	GTCCTACTCT	420
ACTTTCCCAG GTTTTGTTT	CTGGAGGGAC	CCCAAGAGTG	GCTCCTGGTA	CGTTGAGACC	480
CTGGACGACA TCTTTGAGC	A GTGGGCTCAC	TCTGAAGACC	TGCAGTCCCT	CCTGCTTAGG	540
GTCGCTAATG CTGTTTCGG	r gaaagggatt	TATAAACAGA	TGCCTGGTTG	CTTTAATTTC	600
CTCCGGAAAA AACTTTTCT	TTAAAACATC	ATAAGGCAG			639

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 203 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Val	Leu	Ala	Leu	Leu	Glu	Leu	Ala	Arg	Gln	Asp	His	Gly	Ala	Leu
1				5					10					15	
Asp	Cys	Cys	Val	Val	Val	Ile	Leu	Ser	His	Gly	Cys	Gln	Ala	Ser	His
			20					25					30		
Leu	Gln	Phe	Pro	Gly	Ala	Val	Tyr	Gly	Thr	Asp	Gly	Cys	Pro	Val	Ser
		35					40					45			
Val	Glu	Lys	Ile	Val	Asn	Ile	Phe	Asn	Gly	Thr	Ser	Cys	Pro	Ser	Leu
	50					55					60				
Glv	Glv	Lvs	Pro	Lys	Leu	?he	Phe	Ile	Gln	Ala	Cys	Gly	Gly	Glu	Gln

75 65 Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu Asp Glu Ser 90 85 Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln Glu Gly Leu 105 100 Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro Thr Pro Ser 120 Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val Ser Trp Arg 135 130 Asp Pro Lys Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp Asp Ile Phe 155 150 Glu Gln Trp Ala His Ser Glu Asp Leu Gln Ser Leu Leu Leu Arg Val 170 Ala Asn Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met Pro Gly Cys 190 180 Phe Asn Phe Leu Arg Lys Lys Leu Phe Phe Met .200 195

- (2) INFORMATION FOR SEQ ID NO:5:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTISENSE: NO
 - (v) FRAGMENT TYPE:
 - (vi) ORIGINAL SOURCE:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAACGGGGTA CCGCCATGGA CGAAGCGGAT CGGC

- (2) INFORMATION FOR SEQ ID NO:6:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear



(ii) MOLECUI	E TYPE	: CDNA
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- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (V) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TGCTCTAGAT TAGTGGTGGT GGTGGTGGTG TGATGTTTTA AAGAAAAGTT TTTTCCGGAG

- (2) INFORMATION FOR SEQ ID NO:7:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGCTCTTTT TCATCCAGGC CGCGGGTGGG GAGCAGAAGA C

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTCTTTCTGC TCCCCACCCG CGGCCTGGAT GAAAAAAGC

(2) INFORMATION	FOR	SEQ	ID	NO:9
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		DA COREDICTICS
1:1	GEOLIENCE	CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGCTCTAGAT	TACTTGTCAT	CGTCGTCCTT	GTAGTCTGAT	GTTTTAAAGT	TAAGTTTTTT	60 66
CCGGAG						

SEQUENCE LISTING

- (1) GENERAL INFORMATION
- (i) APPLICANT: DIXIT, VISHVA M.

HE, WEI-WU

KIKLY, KRISTINE K. RUBEN, STEVEN M.

- (ii) TITLE OF THE INVENTION: INTERLEUKIN-1 BETA CONVERTING ENZYME LIKE APOPTOTIC PROTEASE-6
- (iii) NUMBER OF SEQUENCES: 11
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Ratner & Prestia
 - (B) STREET: P.O. Box 980
 - (C) CITY: Valley Forge
 - (D) STATE: PA
 - (E) COUNTRY: USA
 - (F) ZIP: 19482
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/352,936
 - (B) FILING DATE: 08-MAY-1997
 - (C) CLASSIFICATION: UNKNOWN
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 60/013, 961
 - (B) FILING DATE: 05-JUN-1996
 - (A) APPLICATION NUMBER: 60/020,344
 - (B) FILING DATE: 23-MAY-1996
 - (A) APPLICATION NUMBER: 60/017,949
 - (B) FILING DATE: 20-MAY-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Prestia, Paul F
 - (B) REGISTRATION NUMBER: 23,031
 - (C) REFERENCE/DOCKET NUMBER: p50483-2
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 610-407-0700
 - (B) TELEFAX: 610-407-0700
 - (C) TELEX: 346169
 - (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 416 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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ě	1et	Asn	G1	u Z	\la	Asp	Arg	, Ar	g !	Leu	Le	u.	Arg	Arg	Сā	s A	Arg	Leu	Arg 15	Le	u
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	7 ~~	50 G17	, 5	- ~	Gln	Ala	Le	u P	ro	Leu	2	ne	Ile	Ser	- C	ys	Leu	Glu	Ası	2 T	nr O
	65	- Glr	n A.	SD	Met	Let	, Al	a S	er	Phe	. I.,	eu	Arg	Thi	- A	sn	Arg	Gln	. Al. 95	a G	тА
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	Λ	.~ ⊃h	20	Ser	⊥¤ Se	u r Le	eu H	is	Phe	. Me	T	/al	31	u Va	al :	Lys	G1;	y As 5	ייי פ	eu '	rnr
	Al	.a L	ys	195 Lys	s Me	ات ۷	al I	eu	Ala 215	a Le	2.12	Le	i Gl	.u 14	eu.	Ala 220	Ar	g Gl	n A	sp	als
# #! #:	G1	2 Ly A	10 la	Le	ı As	sp C	ys 🤇	Cys 230	Va.	l Va	a l	Va.	l Il	.e L 2	eu 35	Ser	Hi.	s Gl	.у С	ys	240
	22 A.	25 La S	er	Hi.	s Le	eu G	ln !	?he	Pr	o G:	LΥ	A1	a Va 25	11 T	ĀL	Gl _y	/ Th	r As	50 G 2	±y 55	Cys
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	P	ro S	er	Le	u G	ly G	ly	ГÀг	Pr	o L 2	ys 90	Le	u Pi	ne P	he	Il:	e G1 28	.n A. 15	ia C	.ys	Gly
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	Ą	sp (290 31u	Se	er P	ro í	Gly	Ser	As	n P	,20	G)	_u }	ro ?	Asp 315	A±	a Ti	nr s	<u> </u>	rile Cou	Gln 320
	3	ous Blu (Gly		eu A	rg	Thr 325	Phe	: As	g de	ln		eu A 3	. sp :	ala -			er o	ei :1,,	335 Dha	Pro Val
	7	nh -	Pro	5.	er 3	Asp 340	ile	şhe	· 17	al S	Ser	3	yr S 45	er '		27. 	.e =	10 0	;-/ ;50 ;5.~	Lau	Val Asp
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Asp Ile Phe Glu Gln Ala His Ser Glu Asp Leu Gln Selou Leu 375 380

Leu Arg Val Ala Asn Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met 390 395 400

Pro Gly Cys Phe Asn Phe Leu Arg Lys Leu Phe Phe Lys Thr Ser 410

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1578 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: CONA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCCATGGACG AAGCGGATCG GCGGCTCCTG CGGCGGTGCC GGCTGCGGCT GGTGGAAGAG CTGCAGGTGG ACCAGCTCTG GGACGTCCTG CTGAGCCGCG AGCTGTTCAG GCCCCATATG 120 ATCGAGGACA TCCAGCGGGC AGGCTCTGGA TCTCGGCGGG ATCAGGCCAG GCAGCTGATC 130 ATAGATOTGG AGACTOGAGG GAGTCAGGCT STTCSTTTGT TCATCTCCTG CTTAGAGGAC 240 ACAGGCCAGG ACATGCTGGC TTCGTTTCTG CGAACTAACA GGCAAGCAGG AAAGTTGTCG 300 AAGCCAACCC TAGAAAACCT TACCCCAGTG GTGCTCAGAC CAGAGATTCG CAAACCAGAG 360 GTTCTCAGAC CGGAAACACC CAGACCAGTG GACATTGGTT CTGGAGGATT CGGTGATGTC 420 GGTGCTCTTG AGAGTTTGAG GGGAAATGCA GATTTGGCTT ACATCCTGAG CATGGAGCCC 480 TGTGGCCACT GCCTCATTAT CAACAATGTG AACTTCTGCC GTGAGTCCGG GCTCCGCACC 540 CGCACTGGCT CCAACATCGA CTGTGAGAAG TTGCGGCGTC GCTTCTCCTC GCTGCATTTC 600 ATGGTGGAGG TGAAGGGCGA CCTGACTGCC AAGAAAATGG TGCTGGCTTT GCTGGAGCTG 660 GCGCGGCAGG ACCACGGTGC TCTGGACTGC TGCGTGGTGG TCATTCTCTC TCACGGCTGT 720 CAGGCCAGCC ACCTGCAGTT CCCAGGGGCT GTCTACGGCA CAGATGGATG CCCTGTGTCG 780 GTCGAGAAGA TTGTGAACAT CTTCAATGGG ACCAGCTGCC CCAGCCTGGG AGGGAAGCCC AAGCTCTTTT TCATCCAGGC CTGTGGTGGG GAGCAGAAAG ACCATGGGTT TGAGGTGGCC 900 TCCACTTCCC CTGAAGACGA GTCCCCTGGC AGTAACCCCG AGCCAGATGC CACCCCGTTC ·960 CAGGAAGGTT TGAGGACCTT CGACCAGCTG GACGCCATAT CTAGTTTGCC CACACCCAGT 1020 GACATOTTEG TGTCCTACTC TACTTTCCCA GGTTTTGTTT CCTGGAGGGA CCCCAAGAGT 1080 GGCTCCTGGT ACGTTGAGAC CCTGGACGAC ATCTTTGAGC AGTGGGCTCA CTCTGAAGAC 1140 CTGCAGTCCC TCCTGCTTAG GGTCGCTAAT GCTGTTTCGG TGAAAGGGAT TTATAAACAG 1200 ATGCCTGGTT GCTTTAATTT CCTCCGGAAA AAACTTTTCT TTAAAAACATC ATAAGGCCAG 1260 GGCCCCTCAC CCTGCCTTAT CTTGCACCCC AAAGCTTTCC TGCCCCAGGC CTGAAAGAGG CTGAGGCCTG GACTTTCCTG CAACTCAAGG ACTTTGNAGC CGGCACAGGG TCTGCTCTTT CTCTGCCAGT GACAGACAGG CTCTTAGCAG CTTCCAGATT GACGACAAGT GCTGAACAGT GGAGGAAGAG GGACAGATGA ATGCCGTGGA TTGCACGTGG NCTCTTGAGC AGTGGCTGGT CCAGGGCTAG TGACTTGGTG TCCCATGATC CCTGTGTTGG TCTCTAGGAG CAGGGATTAA 1560 1578 CCTCTGCACT ACTGACAT

- (2) INFORMATION FOR SEQ ID MC:3:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 639 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: Linear
- (11) MOLECULE TYPE: SONA

(xi) SEQUENCE DESCREPTION: SEQ ID NO:3:

ACTTTCCCAG GTTTTGTTTC CTGGAGGGAC CCCAAGAGTC SCIOCACAGAGTC SCIOCACACAGAGTC SCIOCACAGAGTC SCIOCACAGAGTC SCIOCACACAGAGTC SCIOCACACAGAGTC SCIOCACACACACACACACACACACACACACACACACACAC	ACTTTCCCAG CTGGACGACA	GCGTGGTGGT TCTACGGCAC CCAGCTGCCC AGCAGAAAGA GTAACCCCGA ACGCCATATC GTTTTGTTTC TCTTTGAGCA	AGATGGATGC AGATGGATGC CAGCCTGGGA CCATGGGTTT GCCAGATGCC TAGTTTGCCC CTGGAGGGAC GTGGGCTCAC GAAAGGGATT	CCTGTGTCGG GGGAAGCCCA GAGGTGGCCT ACCCCGTTCC ACACCCAGTG CCCAAGAGTG TCTGAAGACC TATAAACAGA	TCGAAAAGAT AGCTCTTTT CCACTTCCCC AGGAAGGTTT ACATCTTTGT GCTCCTGGTA TGCAGTCCCT	TGTGAACATC CATCCAGGCC TGAAGACGAG GAGGACCTTC GTCCTACTCT CGTTGAGACC CCTGCTTAGG	120 180 240 300 360 420 480 540 600 639
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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

		(x	i) S	EQUE:	NCE	UESC.	KT = T	_0	J-1							
	Met '	Val	Leu	Ala	Leu	Leu	Glu	Leu	Ala	Arg	Gln	ąsA	His	Gly	Ala 15	Leu
	1 Asp	Cvs	Cvs	Val	o Val	Val	Ile	Leu	Ser	His	Gly	Cys	Gln	Ala 30	Ser	His
N.	Leu	Gln	Phe	20 Pro	Gly	Ala	Val	Tyr	Gly	The	ąz£	Gly -	Cys 45	Szo	Val	Ser
	Val	Glú	35 Lys	Ile	Val	Asn	Ile	Phe	Asn	Gly	Thr	Ser	Cys	Pro	Ser	Leu
	Glv	50 Gly	Lys	Pro	Lys	Leu	35 Phe	Phe	:le	Gln	Ala	Cys	Gly	Gly	Glu	Gln 80
	65 Lvs	Asp	His	Gly	?he	70 Glu	Val	Ala	Ser	Thr	Ser	Sio	Glu	Asp	Glu 95	Ser
	Pro	Glv	Ser	Asn	85 Pro	Glu	Pro	Asp	Ala	Thr	Pro	?he	Gln	Glu 110	Gly	Leu
	Ara	Thr	Phe	100 Asp	Gln	Leu	Asp	Ala	Ile	Ser	Ser	Leu	Pro	Thr	510	Ser
	Asn	Tle	115	val	Ser	Tyr	Ser	120 Th:	?he	Pro	Gly	Phe	Val	Ser	Trp	Arg
	Aen	130	i Tivs	s Ser	: Gly	/ Ser	135 Trp	Tyr	· Val	L Gl	ı Thr	Leu	. Asp	Asp	Ile	?he 160
	145	Glo	י ביי	o Ala	ı His	150 s Ser) : Glu	. Asp	let	ı Gl:	ı Ser	: Leu	ı Lev	ı Lev	1 Arg	y Val
	719	. 32.	 - 31.	a 7a.	169 1 3e :	5 r Val	L Lys	s Gly	, II.	e Ty:	r Tās	s Glr	ı Met	220	Gly	, Cys
				180 e Le)			s le	: 25	5 e ?h				150	,	
	2116	:	19	5		, <u>.</u>	-	20	0	יור ב	. .					

- (2) INFORMATION FOR SEQ ID NO:5:
- (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 34 base pairs

	(B) TYPE: nucleic roid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULZ TYPE: CDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	34
G	AACGGGGTA CCGCCATGGA CGAAGCGGAT CGGC	
	(2) INFORMATION FOR SEQ ID NO:6:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 60 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
٠.	(ii) MOLECULE TYPE: CDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:	60
	TGCTCTAGAT TAGTGGTGGT GGTGGTGGTG TGATGTTTTA AAGAAAAGTT TTTTCCGGAG	
	(2) INFORMATION FOR SEQ ID NO:7:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 41 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
juli ≅	(ii) MOLZCULE TYPE: GDNA	,
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:	41
	AAGCTCTTTT TCATCCAGGC CGCGGGTGGG GAGCAGAAGA C	
	(2) INFORMATION FOR SEQ ID NO:8:	
ļ-ā:	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	3'
	GTCTTTCTGC TCCCCACCCG CGGCCTGGAT GAAAAAAGC	,
	(2) INFORMATION FOR SEQ ID NO:9:	
	(1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 66 base pairs (B) TYPE: nucleic acid	

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
TGCTCTAGAT TACTTGTCAT CGTCGTCCTT GTAGTCTGAT GTTTTAAAGT TAAGTTTTTT CCGGAG
(2) INFORMATION FOR SEQ ID NO:10:
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 5 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
Gln Ala Cys Arg Gly 1 5
(2) INFORMATION FOR SEQ ID NC:11:
(2) INFORMATION TO (2) INFORMATION TO (2) INFORMATION TO (3) SEQUENCE CHARACTERISTICS: (A) LENGTH: S amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TCPOLOGY: linear
(ii) MCLECULE TYPE: protein
(x1) SEQUENCE DESCRIPTION: SEQ ID NO:11:
(xi) SEQUENCE DESCRIPTION: SEQ 13 NO.11. Gin Ala Cys Gly Gly 1